# CEDARO Analysis of STAPHBAB-C5R

### Background

The "CERMEL Data Repository" (CEDARO) aims to archive data of all research projects performed at CERMEL. A detailed description of the repository is available from the CEDARO team (cedaro@cermel.org). Before archiving, a codebook and an anomyized dataset are generated. In addition, a basic statistical analysis is performed to ensure that the data in the publication corresponds to the submitted dataset. Typically, only data from the abstract is verified, but it may also include other results from the publication. An analysis report comparing the original published results with that of the CEDARO analysis is generated and sent to the investigator who submitted the data set. The CEDARO team will follow-up on any descripancies to make sure that the analysis and data are valid.

#### **Publication**

#### Reference

Schaumburg F, Witten A, Flamen A, Stoll M, Alabi AS, Kremsner PG, Löffler B, Zipfel PF, Velavan TP, Peters G. Complement 5a Receptor Polymorphisms Are Associated With Panton-Valentine Leukocidin-positive Staphylococcus aureus Colonization in African Pygmies. Clin Infect Dis. 2019 Feb 15;68(5):854-856.

DOI: 10.1093/cid/ciy666 Pubmed ID: 30192927 Pubmed Central ID: NA

#### Abstract

Panton-Valentine leukocidin (PVL) is common in African Staphylococcus aureus and can be associated with skin and soft tissue infection. PVL-positive S. aureus colonization is associated with a variant of complement receptor 5a, the cellular target of the lukS PVL subunit.

### Analysis

#### Section 1

"The recruited Babongo (n=107) had a median age of 13 years (range: 0.75–59) and a balanced ratio of females to males (50 vs 57, respectively). The overall colonization rate was 68.2% (n=73), with a clear age-dependent colonization pattern (with the highest colonization in teenagers). Volunteers were colonized in the nose (n=50), nose and throat (n=15), nose and wound (n=2), throat (n=5), and throat and wound (n=1). None of the wounds showed signs or symptoms of infection. Of the 73 carriers, 33 (45.2%) were colonized with PVL-positive S.aureus and 40 (54.8%) with a PVL-negative isolate ".

Table 1: Section 1 results

Variables	CEDARO P		Discrepancy	
Recruited	107	107	no	
Median age	13 (0.75-59)	$13 \ (0.75-59)$	no	
F	50 (47%)	50 (47%)	no	
M	57 (53%)	57 (53%)	no	
Colonization (no)	34 (31.8%)	34 (31.8%)	no	
Colonization (yes)	73~(68.2%)	73~(68.2%)	no	
PVL_colonized(no)	40 (54.8%)	40 (54.8%)	no	
PVL_colonized (yes)	33~(45.2%)	33~(45.2%)	no	
Nose	50	50	no	
Nose and Throat	15	15	no	
Throat	5	5	no	
Wound	1	1	no	
Wound and Nose	2	2	no	
Wound and Throat	1	1	no	

### Section 2

"After removing duplicate isolates, the final dataset consisted of 85 S.aureus isolates. The predominant ST were ST152 (n = 26,73.1% PVL-positive), ST2788 (n=20, 5% PVL-positive isolates), and ST6 (n = 8, no PVL-positive isolates). Spa types associated with ST152 were t127 (n = 7), t355 (n = 14), t2784 (n = 2), and t3636 (n = 3). Other STs were less diverse in terms of spa types, such as ST2788 (t189, n = 20) and ST6 (t1476, n = 8).

The isolates were resistant to penicillin (n=64, 75.3%), trimethoprim/sulfamethoxazol (n = 14, 16.5%), and tetracycline (n = 11, 12.9%)".

Table 2: Section 2 results

Variables	CEDARO	Published	Discrepancy
Number of isolates	85	85	no
ST152 (PVL-positive)	26 (73.1%)	26 (73.1%)	no
ST2788 (PVL-positive isolates)	20 (5%)	20 (5%)	no
ST6 (no PVL-positive isolates)	8	8	no
t127	7	7	no
t355	14	14	no
t2784	2	2	no
t3636	3	3	no
t189	20	20	no
t1476	8	8	no
Resistant to penicillin	64~(75.3%)	64~(75.3%)	no
Resistant to trimethoprim	14(16.5%)	14(16.5%)	no
Resistant to tetracyline	11 (12.9%)	11 (12.9%)	no

### Section 3

Table 3: Section 3 results

		PVL positive S.aureus						
		yes			no			
$\mathrm{SNPs}$	Genotype	CEDARO	Publ.	Discrep.	CEDARO	Publ.	Discrep.	
SNP_rs11880097_ref_G	TT	28	26	yes	21	21	no	
$SNP_rs11880097_ref_G$	$\operatorname{GT}$	2	2	no	10	11	yes	
$SNP_rs11880097_ref_G$	GG	0	0	no	3	3	no	
$SNP_rs11880097_ref_G$	${ m T}$	58	54	yes	52	53	yes	
$SNP\_rs11880097\_ref\_G$	G	2	2	no	16	17	yes	
$SNP\_rs150649665\_ref\_C$	CC	31	31	no	30	30	no	
$SNP\_rs150649665\_ref\_C$	CA	1	1	no	6	7	yes	
$SNP\_rs150649665\_ref\_C$	AA	0	0	no	1	1	no	
$SNP\_rs150649665\_ref\_C$	$^{\mathrm{C}}$	63	63	no	66	67	yes	
$SNP\_rs150649665\_ref\_C$	A	1	1	no	8	9	yes	
SNP_rs187635721_ref_G	GG	27	27	no	23	23	no	
$SNP_rs187635721_ref_G$	$\operatorname{GT}$	2	2	no	5	6	yes	
$SNP\_rs187635721\_ref\_G$	$\operatorname{TT}$	0	0	no	3	3	no	
$SNP\_rs187635721\_ref\_G$	G	56	56	no	51	52	yes	
$SNP\_rs187635721\_ref\_G$	${ m T}$	2	2	no	11	12	yes	

## Repository details

- CEDARO acronym: STAPHBAB-C5R
- CEDARO ID: NA
- $\bullet~$  Date of report: 2019-10-11
- Analysis performed by: Eddy Mbena
- Analysis supervised by: Fabrice Mougeni & Bertrand Lell
- Raw data supplied by: Frieder Schaumburg
- Code repository: https://gitlab.com/MBENA/staphbab-c5r
- Local storage path: NAS